



"Express Mail" mailing number: EV372405096US

Date of Deposit April 15, 2004

I hereby certify that this correspondence is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. 1.10 on the date indicated above and is addressed to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Patty Wilson
Patty Wilson

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Daniel et al.

Group Art Unit: 1623

Serial No.: 09/516,728

Examiner: Bansal, G.

Filed: March 1, 2000

Docket No.: 1242/12/2 CIP

Confirmation No.: 2723

For: MODULATION OF ENDOTHELIAL CELL SURFACE RECEPTOR ACTIVITY IN
THE REGULATION OF ANGIOGENESIS

**STATEMENT THAT SUBSTITUTE SEQUENCE LISTING AND
COMPUTER READABLE COPY ARE THE SAME**

Commissioner for Patents
Washington, D.C. 20231

Sir:

In accordance with 37 C.F.R. § 1.821(f), applicants hereby state that the Substitute Sequence Listing information recorded in computer readable form is identical to the written Substitute Sequence Listing on paper.

The Commissioner is hereby authorized to charge any deficiency or credit any overpayment associated with the filing of this correspondence to Deposit Account Number **50-0426**.

Respectfully submitted,
JENKINS, WILSON & TAYLOR, P.A.

Date: April 15, 2004

By:

Christopher P. Perkins
Registration No. 52,111

Customer No.: **25297**
1242/12/2 CIP CPP/ptw



SUBSTITUTE SEQUENCE LISTING

<110> VANDERBILT UNIVERSITY
DANIEL, THOMAS
TAKAHASHI, TAKAMUNE
MERNAUGH, RAYMOND

<120> MODULATION OF ENDOTHELIAL CELL SURFACE RECEPTOR ACTIVITY IN THE
REGULATION OF ANGIOGENESIS

<130> 1242/12/2 CIP

<140> 09/516,728
<141> 2000-03-01

<150> US 09/152,160
<151> 1998-09-10

<160> 4

<170> PatentIn version 3.2

<210> 1
<211> 8
<212> PRT
<213> Homo sapiens

<400> 1

Gln Ser Arg Asp Thr Glu Val Leu
1 5

<210> 2
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Artifical peptide spacer

<400> 2

Leu Ala Leu Ala
1

<210> 3
<211> 5117
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (350)..(4363)

<300>
 <301> Ostman,A., Yang,Q. and Tonks,N.K.
 <302> Expression of DEP-1, a receptor-like
 protein-tyrosine-phosphatase, is enhanced with increasing cell
 density
 <303> Proc. Natl. Acad. Sci. U.S.A.
 <304> 91
 <305> 21
 <306> 9680-9684
 <307> 1994-10-11
 <308> U10886
 <309> 1994-06-15
 <313> (1)..(5117)

 <400> 3
 cccagccgc atgacgcgcg gaggaggcag cgggacgagc gcgggagccg ggaccgggta 60
 gccgcgcgct ggggggtgggc gccgctcgtc ccgccccgcg aagcccctgc gcgctcaggg 120
 acgcggcccc ccgcggcag ccgcgctagg ctccggcgtg tggccgcggc cgccgcgcgcg 180
 ctgccatgtc tccgggcaag ccggggcggg cggagcgggg acgaggcgga ccggctggcg 240
 gaggaggagg cgaaggagac ggcaggaggc ggcgacgacg gtgcccgggc tcgggcgcac 300
 ggcgggggccc gattcgcgcg tccggggcac gttccagggc gcgcggggc atg aag ccg 358
 Met Lys Pro
 1
 gcg gcg cgg gag gcg cgg ctg cct ccg cgc tgc ccc ggg ctg cgc tgg 406
 Ala Ala Arg Glu Ala Arg Leu Pro Pro Arg Ser Pro Gly Leu Arg Trp
 5 10 15
 gcg ctg ccg ctg ctg ctg ctg ctg ctg cgc ctg ggc cag atc ctg tgc 454
 Ala Leu Pro Leu Leu Leu Leu Leu Leu Arg Leu Gly Gln Ile Leu Cys
 20 25 30 35
 gca ggt ggc acc cct agt cca att cct gac cct tca gta gca act gtt 502
 Ala Gly Gly Thr Pro Ser Pro Ile Pro Asp Pro Ser Val Ala Thr Val
 40 45 50
 gcc aca ggg gaa aat ggc ata acg cag atc agc agt aca gca gaa tcc 550
 Ala Thr Gly Glu Asn Gly Ile Thr Gln Ile Ser Ser Thr Ala Glu Ser
 55 60 65
 ttt cat aaa cag aat gga act gga aca cct cag gtg gaa aca aac acc 598
 Phe His Lys Gln Asn Gly Thr Gly Thr Pro Gln Val Glu Thr Asn Thr
 70 75 80
 agt gag gat ggt gaa agc tct gga gcc aac gat agt tta aga aca cct 646
 Ser Glu Asp Gly Glu Ser Ser Gly Ala Asn Asp Ser Leu Arg Thr Pro
 85 90 95
 gaa caa gga tct aat ggg act gat ggg gca tct caa aaa act ccc agt 694
 Glu Gln Gly Ser Asn Gly Thr Asp Gly Ala Ser Gln Lys Thr Pro Ser
 100 105 110 115

agc act ggg ccc agt cct gtg ttt gac att aaa gct gtt tcc atc agt Ser Thr Gly Pro Ser Pro Val Phe Asp Ile Lys Ala Val Ser Ile Ser	742
120 125 130	
cca acc aat gtg atc tta act tgg aaa agt aat gac aca gct gct tct Pro Thr Asn Val Ile Leu Thr Trp Lys Ser Asn Asp Thr Ala Ala Ser	790
135 140 145	
gag tac aag tat gta gta aag cat aag atg gaa aat gag aag aca att Glu Tyr Lys Tyr Val Val Lys His Lys Met Glu Asn Glu Lys Thr Ile	838
150 155 160	
act gtt gtg cat caa cca tgg tgt aac atc aca ggc tta cgt cca gcg Thr Val Val His Gln Pro Trp Cys Asn Ile Thr Gly Leu Arg Pro Ala	886
165 170 175	
act tca tat gta ttc tcc atc act cca gga ata ggc aat gag act tgg Thr Ser Tyr Val Phe Ser Ile Thr Pro Gly Ile Gly Asn Glu Thr Trp	934
180 185 190 195	
gga gat ccc aga gtc ata aaa gtc atc aca gag ccg atc cca gtt tct Gly Asp Pro Arg Val Ile Lys Val Ile Thr Glu Pro Ile Pro Val Ser	982
200 205 210	
gat ctc cgt gtt gcc ctc acg ggt gtg agg aag gct gct ctc tcc tgg Asp Leu Arg Val Ala Leu Thr Gly Val Arg Lys Ala Ala Leu Ser Trp	1030
215 220 225	
agc aat ggc aat ggc acc gcc tcc tgc cgg gtt ctt ctt gaa agc att Ser Asn Gly Asn Gly Thr Ala Ser Cys Arg Val Leu Leu Glu Ser Ile	1078
230 235 240	
gga agc cat gag gag ttg act caa gac tca aga ctt cag gtc aat atc Gly Ser His Glu Glu Leu Thr Gln Asp Ser Arg Leu Gln Val Asn Ile	1126
245 250 255	
tcg gac ctg aag cca ggg gtt caa tac aac atc aac ccg tat ctt cta Ser Asp Leu Lys Pro Gly Val Gln Tyr Asn Ile Asn Pro Tyr Leu Leu	1174
260 265 270 275	
caa tca aat aag aca aag gga gac ccc ttg ggc aca gaa ggt ggc ttg Gln Ser Asn Lys Thr Lys Gly Asp Pro Leu Gly Thr Glu Gly Gly Leu	1222
280 285 290	
gat gcc agc aat aca gag aga agc cgg gca ggg agc ccc acc gcc cct Asp Ala Ser Asn Thr Glu Arg Ser Arg Ala Gly Ser Pro Thr Ala Pro	1270
295 300 305	
gtg cat gat gag tcc ctc gtg gga cct gtg gac cca tcc tcc ggc cag Val His Asp Glu Ser Leu Val Gly Pro Val Asp Pro Ser Ser Gly Gln	1318
310 315 320	
cag tcc cga gac acg gaa gtc ctg ctt gtc ggg tta gag cct ggc acc Gln Ser Arg Asp Thr Glu Val Leu Leu Val Gly Leu Glu Pro Gly Thr	1366
325 330 335	

cga tac aat gcc acc gtt tat tcc caa gca gcg aat ggc aca gaa gga Arg Tyr Asn Ala Thr Val Tyr Ser Gln Ala Ala Asn Gly Thr Glu Gly 340 345 350 355	1414
cag ccc cag gcc ata gag ttc agg aca aat gct att cag gtt ttt gac Gln Pro Gln Ala Ile Glu Phe Arg Thr Asn Ala Ile Gln Val Phe Asp 360 365 370	1462
gtc acc gct gtg aac atc agt gcc aca agc ctg acc ctg atc tgg aaa Val Thr Ala Val Asn Ile Ser Ala Thr Ser Leu Thr Leu Ile Trp Lys 375 380 385	1510
gtc agc gat aac gag tcg tca tct aac tat acc tac aag ata cat gtg Val Ser Asp Asn Glu Ser Ser Ser Asn Tyr Thr Tyr Lys Ile His Val 390 395 400	1558
gcg ggg gag aca gat tct tcc aat ctc aac gtc agt gag cct cgc gct Ala Gly Glu Thr Asp Ser Ser Asn Leu Asn Val Ser Glu Pro Arg Ala 405 410 415	1606
gtc atc ccc gga ctc cgc tcc agc acc ttc tac aac atc aca gtg tgt Val Ile Pro Gly Leu Arg Ser Ser Thr Phe Tyr Asn Ile Thr Val Cys 420 425 430 435	1654
cct gtc cta ggt gac atc gag ggc acg ccg ggc ttc ctc caa gtg cac Pro Val Leu Gly Asp Ile Glu Gly Thr Pro Gly Phe Leu Gln Val His 440 445 450	1702
acc ccc cct gtt cca gtt tct gac ttc cga gtg aca gtg gtc agc acg Thr Pro Pro Val Pro Val Ser Asp Phe Arg Val Thr Val Val Ser Thr 455 460 465	1750
acg gag atc ggc tta gca tgg agc agc cat gat gca gaa tca ttt cag Thr Glu Ile Gly Leu Ala Trp Ser Ser His Asp Ala Glu Ser Phe Gln 470 475 480	1798
atg cat atc aca cag gag gga gct ggc aat tct cgg gta gaa ata acc Met His Ile Thr Gln Glu Gly Ala Gly Asn Ser Arg Val Glu Ile Thr 485 490 495	1846
acc aac caa agt att atc att ggt ggc ttg ttc cct gga acc aag tat Thr Asn Gln Ser Ile Ile Ile Gly Gly Leu Phe Pro Gly Thr Lys Tyr 500 505 510 515	1894
tgc ttt gaa ata gtt cca aaa gga cca aat ggg act gaa ggg gca tct Cys Phe Glu Ile Val Pro Lys Gly Pro Asn Gly Thr Glu Gly Ala Ser 520 525 530	1942
cgg aca gtt tgc aat aga act gtt ccc agt gca gtg ttt gac atc cac Arg Thr Val Cys Asn Arg Thr Val Pro Ser Ala Val Phe Asp Ile His 535 540 545	1990
gtg gtc tac gtc acc acc acg gag atg tgg ctg gac tgg aag agc cct Val Val Tyr Val Thr Thr Thr Glu Met Trp Leu Asp Trp Lys Ser Pro 550 555 560	2038

gac ggt gct tcc gag tat gtc tac cat tta gtc ata gag tcc aag cat Asp Gly Ala Ser Glu Tyr Val Tyr His Leu Val Ile Glu Ser Lys His 565 570 575	2086
ggc tct aac cac aca agc acg tat gac aaa gcg att act ctc cag ggc Gly Ser Asn His Thr Ser Thr Tyr Asp Lys Ala Ile Thr Leu Gln Gly 580 585 590 595	2134
ctg att ccg ggc acc tta tat aac atc acc atc tct cca gaa gtg gac Leu Ile Pro Gly Thr Leu Tyr Asn Ile Thr Ile Ser Pro Glu Val Asp 600 605 610	2182
cac gtc tgg ggg gac ccc aac tcc act gca cag tac aca cgg ccc agc His Val Trp Gly Asp Pro Asn Ser Thr Ala Gln Tyr Thr Arg Pro Ser 615 620 625	2230
aat gtg tcc aac att gat gta agt acc aac acc aca gca gca act tta Asn Val Ser Asn Ile Asp Val Ser Thr Asn Thr Thr Ala Ala Thr Leu 630 635 640	2278
agt tgg cag aac ttt gat gac gcc tct ccc acg tac tcc tac tgc ctt Ser Trp Gln Asn Phe Asp Asp Ala Ser Pro Thr Tyr Ser Tyr Cys Leu 645 650 655	2326
ctt att gag aag gct gga aat tcc agc aac gca aca caa gta gtc acg Leu Ile Glu Lys Ala Gly Asn Ser Ser Asn Ala Thr Gln Val Val Thr 660 665 670 675	2374
gac att gga att act gac gct aca gtc act gaa tta ata cct ggc tca Asp Ile Gly Ile Thr Asp Ala Thr Val Thr Glu Leu Ile Pro Gly Ser 680 685 690	2422
tca tac aca gtg gag atc ttt gca caa gta ggg gat ggg atc aag tca Ser Tyr Thr Val Glu Ile Phe Ala Gln Val Gly Asp Gly Ile Lys Ser 695 700 705	2470
ctg gaa cct ggc cgg aag tca ttc tgt aca gat cct gcg tcc atg gcc Leu Glu Pro Gly Arg Lys Ser Phe Cys Thr Asp Pro Ala Ser Met Ala 710 715 720	2518
tcc ttc gac tgc gaa gtg gtc ccc aaa gag cca gcc ctg gtt ctc aaa Ser Phe Asp Cys Glu Val Val Pro Lys Glu Pro Ala Leu Val Leu Lys 725 730 735	2566
tgg acc tgc cct cct ggc gcc aat gca ggc ttt gag ctg gag gtc agc Trp Thr Cys Pro Pro Gly Ala Asn Ala Gly Phe Glu Leu Glu Val Ser 740 745 750 755	2614
agt gga gcc tgg aac aat gcg acc cac ctg gag agc tgc tcc tct gag Ser Gly Ala Trp Asn Asn Ala Thr His Leu Glu Ser Cys Ser Ser Glu 760 765 770	2662
aat ggc act gag tat aga acg gaa gtc acg tat ttg aat ttt tct acc Asn Gly Thr Glu Tyr Arg Thr Glu Val Thr Tyr Leu Asn Phe Ser Thr 775 780 785	2710

tcg tac aac atc agc atc acc act gtg tcc tgt gga aag atg gca gcc Ser Tyr Asn Ile Ser Ile Thr Thr Val Ser Cys Gly Lys Met Ala Ala 790 795 800	2758
ccc acc cgg aac acc tgc act act ggc atc aca gat ccc cct cct cca Pro Thr Arg Asn Thr Cys Thr Thr Gly Ile Thr Asp Pro Pro Pro Pro 805 810 815	2806
gat gga tcc cct aat att aca tct gtc agt cac aat tca gta aag gtc Asp Gly Ser Pro Asn Ile Thr Ser Val Ser His Asn Ser Val Lys Val 820 825 830 835	2854
aag ttc agt gga ttt gaa gcc agc cac gga ccc atc aaa gcc tat gct Lys Phe Ser Gly Phe Glu Ala Ser His Gly Pro Ile Lys Ala Tyr Ala 840 845 850	2902
gtc att ctc acc acc ggg gaa gct ggt cac cct tct gca gat gtc ctg Val Ile Leu Thr Thr Gly Glu Ala Gly His Pro Ser Ala Asp Val Leu 855 860 865	2950
aaa tac acg tat gac gat ttc aaa aag gga gcc tca gat act tat gtg Lys Tyr Thr Tyr Asp Asp Phe Lys Lys Gly Ala Ser Asp Thr Tyr Val 870 875 880	2998
aca tac ctc ata aga aca gaa gaa aag gga cgt tct cag agc ttg tct Thr Tyr Leu Ile Arg Thr Glu Glu Lys Gly Arg Ser Gln Ser Leu Ser 885 890 895	3046
gaa gtt ttg aaa tat gaa att gac gtt ggg aat gag tca acc aca ctt Glu Val Leu Lys Tyr Glu Ile Asp Val Gly Asn Glu Ser Thr Thr Leu 900 905 910 915	3094
ggt tat tac aat ggg aag ctg gaa cct ctg ggc tcc tac cgg gct tgt Gly Tyr Tyr Asn Gly Lys Leu Glu Pro Leu Gly Ser Tyr Arg Ala Cys 920 925 930	3142
gtg gct ggc ttc acc aac att acc ttc cac cct caa aac aag ggg ctc Val Ala Gly Phe Thr Asn Ile Thr Phe His Pro Gln Asn Lys Gly Leu 935 940 945	3190
att gat ggg gct gag agc tat gtg tcc ttc agt cgc tac tca gat gct Ile Asp Gly Ala Glu Ser Tyr Val Ser Phe Ser Arg Tyr Ser Asp Ala 950 955 960	3238
gtt tcc ttg ccc cag gat cca ggt gtc atc tgt gga gcg gtt ttt ggc Val Ser Leu Pro Gln Asp Pro Gly Val Ile Cys Gly Ala Val Phe Gly 965 970 975	3286
tgt atc ttt ggt gcc ctg gtt att gtg act gtg gga ggc ttc atc ttc Cys Ile Phe Gly Ala Leu Val Ile Val Thr Val Gly Gly Phe Ile Phe 980 985 990 995	3334
tgg aga aag aag agg aaa gat gca aag aat aat gaa gtg tcc ttt Trp Arg Lys Lys Arg Lys Asp Ala Lys Asn Asn Glu Val Ser Phe 1000 1005 1010	3379

tct caa att aaa cct	aaa aaa tct aag tta	atc aga gtg gag aat	3424
Ser Gln Ile Lys Pro	Lys Lys Ser Lys Leu	Ile Arg Val Glu Asn	
1015	1020	1025	
ttt gag gcc tac ttc	aag aag cag caa gct	gac tcc aac tgt ggg	3469
Phe Glu Ala Tyr Phe	Lys Lys Gln Gln Ala	Asp Ser Asn Cys Gly	
1030	1035	1040	
ttc gca gag gaa tac	gaa gat ctg aag ctt	gtt gga att agt caa	3514
Phe Ala Glu Glu Tyr	Glu Asp Leu Lys Leu	Val Gly Ile Ser Gln	
1045	1050	1055	
cct aaa tat gca gca	gaa ctg gct gag aat	aga gga aag aat cgc	3559
Pro Lys Tyr Ala Ala	Glu Leu Ala Glu Asn	Arg Gly Lys Asn Arg	
1060	1065	1070	
tat aat aat gtt ctg	ccc tat gat att tcc	cgt gtc aaa ctt tcg	3604
Tyr Asn Asn Val Leu	Pro Tyr Asp Ile Ser	Arg Val Lys Leu Ser	
1075	1080	1085	
gtc cag acc cat tca	acg gat gac tac atc	aat gcc aac tac atg	3649
Val Gln Thr His Ser	Thr Asp Asp Tyr Ile	Asn Ala Asn Tyr Met	
1090	1095	1100	
cct ggc tac cac tcc	aag aaa gat ttt att	gcc aca caa gga cct	3694
Pro Gly Tyr His Ser	Lys Lys Asp Phe Ile	Ala Thr Gln Gly Pro	
1105	1110	1115	
tta ccg aac act ttg	aaa gat ttt tgg cgt	atg gtt tgg gag aaa	3739
Leu Pro Asn Thr Leu	Lys Asp Phe Trp Arg	Met Val Trp Glu Lys	
1120	1125	1130	
aat gta tat gcc atc	att atg ttg act aaa	tgt gtt gaa cag gga	3784
Asn Val Tyr Ala Ile	Ile Met Leu Thr Lys	Cys Val Glu Gln Gly	
1135	1140	1145	
aga acc aaa tgt gag	gag tat tgg ccc tcc	aag cag gct cag gac	3829
Arg Thr Lys Cys Glu	Glu Tyr Trp Pro Ser	Lys Gln Ala Gln Asp	
1150	1155	1160	
tat gga gac ata act	gtg gca atg aca tca	gaa att gtt ctt ccg	3874
Tyr Gly Asp Ile Thr	Val Ala Met Thr Ser	Glu Ile Val Leu Pro	
1165	1170	1175	
gaa tgg acc atc aga	gat ttc aca gtg aaa	aat atc cag aca agt	3919
Glu Trp Thr Ile Arg	Asp Phe Thr Val Lys	Asn Ile Gln Thr Ser	
1180	1185	1190	
gag agt cac cct ctg	aga cag ttc cat ttc	acc tcc tgg cca gac	3964
Glu Ser His Pro Leu	Arg Gln Phe His Phe	Thr Ser Trp Pro Asp	
1195	1200	1205	
cac ggt gtt ccc gac	acc act gac ctg ctc	atc aac ttc cgg tac	4009
His Gly Val Pro Asp	Thr Thr Asp Leu Leu	Ile Asn Phe Arg Tyr	
1210	1215	1220	

ctc gtt cgt gac tac	atg aag cag agt cct	ccc gaa tcg ccg att	4054
Leu Val Arg Asp Tyr	Met Lys Gln Ser Pro	Pro Glu Ser Pro Ile	
1225	1230	1235	
ctg gtg cat tgc agt	gct ggg gtc gga agg	acg ggc act ttc att	4099
Leu Val His Cys Ser	Ala Gly Val Gly Arg	Thr Gly Thr Phe Ile	
1240	1245	1250	
gcc att gat cgt ctc	atc tac cag ata gag	aat gag aac acc gtg	4144
Ala Ile Asp Arg Leu	Ile Tyr Gln Ile Glu	Asn Glu Asn Thr Val	
1255	1260	1265	
gat gtg tat ggg att	gtg tat gac ctt cga	atg cat agg cct tta	4189
Asp Val Tyr Gly Ile	Val Tyr Asp Leu Arg	Met His Arg Pro Leu	
1270	1275	1280	
atg gtg cag aca gag	gac cag tat gtt ttc	ctc aat cag tgt gtt	4234
Met Val Gln Thr Glu	Asp Gln Tyr Val Phe	Leu Asn Gln Cys Val	
1285	1290	1295	
ttg gat att gtc aga	tcc cag aaa gac tca	aaa gta gat ctt atc	4279
Leu Asp Ile Val Arg	Ser Gln Lys Asp Ser	Lys Val Asp Leu Ile	
1300	1305	1310	
tac cag aac aca act	gca atg aca atc tat	gaa aac ctt gcg ccc	4324
Tyr Gln Asn Thr Thr	Ala Met Thr Ile Tyr	Glu Asn Leu Ala Pro	
1315	1320	1325	
gtg acc aca ttt gga	aag acc aat ggt tac	atc gcc taa ttccaaagga	4373
Val Thr Thr Phe Gly	Lys Thr Asn Gly Tyr	Ile Ala	
1330	1335		
ataacctttc tggagtgaac cagaccgtcg caccacagc gaaggcacat gccccgatgt			4433
cgacatgttt ttatatgtct aatatcttaa ttctttgttc tgttttgtga gaactaat			4493
tgagggcatg aagctgcata tgatagatga caaattgggg ctgtcggggg ctgtggatgg			4553
gtggggagca aatcatctgc attcctgatg accaatggga tgaggctact tttttttttt			4613
tcccccttga ggattgcgga aaaccaggaa aagggatcta tgattttttt ttccaaaaca			4673
atttcttttt taaaaagact attttatatg attcacatgc taaagccagg attgtgttgg			4733
gttgaatata ttttaagtat cagaggtcta tttttacctt ctgtgtcttg gaatctagcc			4793
gatggaaaat acctaatgt ggatgatgat tgcgcaggga ggggtacgtg gcacctcttc			4853
cgaatggggt ttctatttga acatgtgcct tttctgaatt atgcttccac aggcaaaact			4913
cagtagagat ctatatTTTT gtactgaatc tcataattgg aatatacgga atatttaa			4973
agtagcttag catcagaggt ttgcttcctc agtaacattt ctgttctcat ttgatcagg			5033
gaggcctctt tgccccggcc ccgcttcccc tgcccccggtg tgatttgtgc tccatttttt			5093
cttccctttt cctcccaagt tttc			5117

<210> 4
 <211> 1337
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Lys Pro Ala Ala Arg Glu Ala Arg Leu Pro Pro Arg Ser Pro Gly
 1 5 10 15

Leu Arg Trp Ala Leu Pro Leu Leu Leu Leu Leu Leu Arg Leu Gly Gln
 20 25 30

Ile Leu Cys Ala Gly Gly Thr Pro Ser Pro Ile Pro Asp Pro Ser Val
 35 40 45

Ala Thr Val Ala Thr Gly Glu Asn Gly Ile Thr Gln Ile Ser Ser Thr
 50 55 60

Ala Glu Ser Phe His Lys Gln Asn Gly Thr Gly Thr Pro Gln Val Glu
 65 70 75 80

Thr Asn Thr Ser Glu Asp Gly Glu Ser Ser Gly Ala Asn Asp Ser Leu
 85 90 95

Arg Thr Pro Glu Gln Gly Ser Asn Gly Thr Asp Gly Ala Ser Gln Lys
 100 105 110

Thr Pro Ser Ser Thr Gly Pro Ser Pro Val Phe Asp Ile Lys Ala Val
 115 120 125

Ser Ile Ser Pro Thr Asn Val Ile Leu Thr Trp Lys Ser Asn Asp Thr
 130 135 140

Ala Ala Ser Glu Tyr Lys Tyr Val Val Lys His Lys Met Glu Asn Glu
 145 150 155 160

Lys Thr Ile Thr Val Val His Gln Pro Trp Cys Asn Ile Thr Gly Leu
 165 170 175

Arg Pro Ala Thr Ser Tyr Val Phe Ser Ile Thr Pro Gly Ile Gly Asn
 180 185 190

Glu Thr Trp Gly Asp Pro Arg Val Ile Lys Val Ile Thr Glu Pro Ile
 195 200 205

Pro Val Ser Asp Leu Arg Val Ala Leu Thr Gly Val Arg Lys Ala Ala
 210 215 220

Leu Ser Trp Ser Asn Gly Asn Gly Thr Ala Ser Cys Arg Val Leu Leu
 225 230 235 240

Glu Ser Ile Gly Ser His Glu Glu Leu Thr Gln Asp Ser Arg Leu Gln
 245 250 255

Val Asn Ile Ser Asp Leu Lys Pro Gly Val Gln Tyr Asn Ile Asn Pro
 260 265 270

Tyr Leu Leu Gln Ser Asn Lys Thr Lys Gly Asp Pro Leu Gly Thr Glu
 275 280 285

Gly Gly Leu Asp Ala Ser Asn Thr Glu Arg Ser Arg Ala Gly Ser Pro
 290 295 300

Thr Ala Pro Val His Asp Glu Ser Leu Val Gly Pro Val Asp Pro Ser
 305 310 315 320

Ser Gly Gln Gln Ser Arg Asp Thr Glu Val Leu Leu Val Gly Leu Glu
 325 330 335

Pro Gly Thr Arg Tyr Asn Ala Thr Val Tyr Ser Gln Ala Ala Asn Gly
 340 345 350

Thr Glu Gly Gln Pro Gln Ala Ile Glu Phe Arg Thr Asn Ala Ile Gln
 355 360 365

Val Phe Asp Val Thr Ala Val Asn Ile Ser Ala Thr Ser Leu Thr Leu
 370 375 380

Ile Trp Lys Val Ser Asp Asn Glu Ser Ser Ser Asn Tyr Thr Tyr Lys
 385 390 395 400

Ile His Val Ala Gly Glu Thr Asp Ser Ser Asn Leu Asn Val Ser Glu
 405 410 415

Pro Arg Ala Val Ile Pro Gly Leu Arg Ser Ser Thr Phe Tyr Asn Ile
 420 425 430

Thr Val Cys Pro Val Leu Gly Asp Ile Glu Gly Thr Pro Gly Phe Leu
 435 440 445

Gln Val His Thr Pro Pro Val Pro Val Ser Asp Phe Arg Val Thr Val
 450 455 460

Val Ser Thr Thr Glu Ile Gly Leu Ala Trp Ser Ser His Asp Ala Glu
 465 470 475 480

Ser Phe Gln Met His Ile Thr Gln Glu Gly Ala Gly Asn Ser Arg Val
 485 490 495

Glu Ile Thr Thr Asn Gln Ser Ile Ile Ile Gly Gly Leu Phe Pro Gly
 500 505 510

Thr Lys Tyr Cys Phe Glu Ile Val Pro Lys Gly Pro Asn Gly Thr Glu
 515 520 525

Gly Ala Ser Arg Thr Val Cys Asn Arg Thr Val Pro Ser Ala Val Phe
 530 535 540

Asp Ile His Val Val Tyr Val Thr Thr Thr Glu Met Trp Leu Asp Trp
 545 550 555 560

Lys Ser Pro Asp Gly Ala Ser Glu Tyr Val Tyr His Leu Val Ile Glu
 565 570 575

Ser Lys His Gly Ser Asn His Thr Ser Thr Tyr Asp Lys Ala Ile Thr
 580 585 590

Leu Gln Gly Leu Ile Pro Gly Thr Leu Tyr Asn Ile Thr Ile Ser Pro
 595 600 605

Glu Val Asp His Val Trp Gly Asp Pro Asn Ser Thr Ala Gln Tyr Thr
 610 615 620

Arg Pro Ser Asn Val Ser Asn Ile Asp Val Ser Thr Asn Thr Thr Ala
 625 630 635 640

Ala Thr Leu Ser Trp Gln Asn Phe Asp Asp Ala Ser Pro Thr Tyr Ser
 645 650 655

Tyr Cys Leu Leu Ile Glu Lys Ala Gly Asn Ser Ser Asn Ala Thr Gln
660 665 670

Val Val Thr Asp Ile Gly Ile Thr Asp Ala Thr Val Thr Glu Leu Ile
675 680 685

Pro Gly Ser Ser Tyr Thr Val Glu Ile Phe Ala Gln Val Gly Asp Gly
690 695 700

Ile Lys Ser Leu Glu Pro Gly Arg Lys Ser Phe Cys Thr Asp Pro Ala
705 710 715 720

Ser Met Ala Ser Phe Asp Cys Glu Val Val Pro Lys Glu Pro Ala Leu
725 730 735

Val Leu Lys Trp Thr Cys Pro Pro Gly Ala Asn Ala Gly Phe Glu Leu
740 745 750

Glu Val Ser Ser Gly Ala Trp Asn Asn Ala Thr His Leu Glu Ser Cys
755 760 765

Ser Ser Glu Asn Gly Thr Glu Tyr Arg Thr Glu Val Thr Tyr Leu Asn
770 775 780

Phe Ser Thr Ser Tyr Asn Ile Ser Ile Thr Thr Val Ser Cys Gly Lys
785 790 795 800

Met Ala Ala Pro Thr Arg Asn Thr Cys Thr Thr Gly Ile Thr Asp Pro
805 810 815

Pro Pro Pro Asp Gly Ser Pro Asn Ile Thr Ser Val Ser His Asn Ser
820 825 830

Val Lys Val Lys Phe Ser Gly Phe Glu Ala Ser His Gly Pro Ile Lys
835 840 845

Ala Tyr Ala Val Ile Leu Thr Thr Gly Glu Ala Gly His Pro Ser Ala
850 855 860

Asp Val Leu Lys Tyr Thr Tyr Asp Asp Phe Lys Lys Gly Ala Ser Asp
865 870 875 880

Thr Tyr Val Thr Tyr Leu Ile Arg Thr Glu Glu Lys Gly Arg Ser Gln
885 890 895

Ser Leu Ser Glu Val Leu Lys Tyr Glu Ile Asp Val Gly Asn Glu Ser
900 905 910

Thr Thr Leu Gly Tyr Tyr Asn Gly Lys Leu Glu Pro Leu Gly Ser Tyr
915 920 925

Arg Ala Cys Val Ala Gly Phe Thr Asn Ile Thr Phe His Pro Gln Asn
930 935 940

Lys Gly Leu Ile Asp Gly Ala Glu Ser Tyr Val Ser Phe Ser Arg Tyr
945 950 955 960

Ser Asp Ala Val Ser Leu Pro Gln Asp Pro Gly Val Ile Cys Gly Ala
965 970 975

Val Phe Gly Cys Ile Phe Gly Ala Leu Val Ile Val Thr Val Gly Gly
980 985 990

Phe Ile Phe Trp Arg Lys Lys Arg Lys Asp Ala Lys Asn Asn Glu Val
995 1000 1005

Ser Phe Ser Gln Ile Lys Pro Lys Lys Ser Lys Leu Ile Arg Val
1010 1015 1020

Glu Asn Phe Glu Ala Tyr Phe Lys Lys Gln Gln Ala Asp Ser Asn
1025 1030 1035

Cys Gly Phe Ala Glu Glu Tyr Glu Asp Leu Lys Leu Val Gly Ile
1040 1045 1050

Ser Gln Pro Lys Tyr Ala Ala Glu Leu Ala Glu Asn Arg Gly Lys
1055 1060 1065

Asn Arg Tyr Asn Asn Val Leu Pro Tyr Asp Ile Ser Arg Val Lys
1070 1075 1080

Leu Ser Val Gln Thr His Ser Thr Asp Asp Tyr Ile Asn Ala Asn
1085 1090 1095

Tyr Met	Pro Gly	Tyr His	Ser	Lys Lys	Asp Phe	Ile	Ala Thr	Gln
1100			1105			1110		
Gly Pro	Leu Pro	Asn Thr	Leu	Lys Asp	Phe Trp	Arg	Met Val	Trp
1115			1120			1125		
Glu Lys	Asn Val	Tyr Ala	Ile	Ile Met	Leu Thr	Lys	Cys Val	Glu
1130			1135			1140		
Gln Gly	Arg Thr	Lys Cys	Glu	Glu Tyr	Trp Pro	Ser	Lys Gln	Ala
1145			1150			1155		
Gln Asp	Tyr Gly	Asp Ile	Thr	Val Ala	Met Thr	Ser	Glu Ile	Val
1160			1165			1170		
Leu Pro	Glu Trp	Thr Ile	Arg	Asp Phe	Thr Val	Lys	Asn Ile	Gln
1175			1180			1185		
Thr Ser	Glu Ser	His Pro	Leu	Arg Gln	Phe His	Phe	Thr Ser	Trp
1190			1195			1200		
Pro Asp	His Gly	Val Pro	Asp	Thr Thr	Asp Leu	Leu	Ile Asn	Phe
1205			1210			1215		
Arg Tyr	Leu Val	Arg Asp	Tyr	Met Lys	Gln Ser	Pro	Pro Glu	Ser
1220			1225			1230		
Pro Ile	Leu Val	His Cys	Ser	Ala Gly	Val Gly	Arg	Thr Gly	Thr
1235			1240			1245		
Phe Ile	Ala Ile	Asp Arg	Leu	Ile Tyr	Gln Ile	Glu	Asn Glu	Asn
1250			1255			1260		
Thr Val	Asp Val	Tyr Gly	Ile	Val Tyr	Asp Leu	Arg	Met His	Arg
1265			1270			1275		
Pro Leu	Met Val	Gln Thr	Glu	Asp Gln	Tyr Val	Phe	Leu Asn	Gln
1280			1285			1290		
Cys Val	Leu Asp	Ile Val	Arg	Ser Gln	Lys Asp	Ser	Lys Val	Asp
1295			1300			1305		

Leu Ile Tyr Gln Asn Thr Thr Ala Met Thr Ile Tyr Glu Asn Leu
1310 1315 1320

Ala Pro Val Thr Thr Phe Gly Lys Thr Asn Gly Tyr Ile Ala
1325 1330 1335